

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 08/439,095  
Source: JFW/6  
Date Processed by STIC: 03/13/2006

***ENTERED***



IFW16

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/439,095

DATE: 03/13/2006

TIME: 14:53:53

Input Set : A:\ 140140279US.SEQLIST.TXT  
 Output Set: N:\CRF4\03132006\H439095.raw

4 <110> APPLICANT: Matsui, Toshimitsu  
 5       Aaronson, Stuart H.  
 6       Pierce, Jacalyn H.  
 8 <120> TITLE OF INVENTION: TYPE ALPHA PLATELET DERIVED GROWTH  
 9       FACTOR RECEPTOR  
 11 <130> FILE REFERENCE: 14014.0279US  
 13 <140> CURRENT APPLICATION NUMBER: 08/439,095  
 14 <141> CURRENT FILING DATE: 1995-05-11  
 16 <150> PRIOR APPLICATION NUMBER: 07/915,884  
 17 <151> PRIOR FILING DATE: 1992-07-20  
 19 <150> PRIOR APPLICATION NUMBER: 07/308,282  
 20 <151> PRIOR FILING DATE: 1989-02-09  
 22 <160> NUMBER OF SEQ ID NOS: 2  
 24 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 26 <210> SEQ ID NO: 1  
 27 <211> LENGTH: 1089  
 28 <212> TYPE: PRT  
 29 <213> ORGANISM: Artificial Sequence  
 31 <220> FEATURE:  
 32 <223> OTHER INFORMATION: Description of Artificial Sequence:/note =  
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 39       20               25                   30  
 40 Asn Glu Asn Glu Lys Val Val Gln Leu Asn Ser Ser Phe Ser Leu Arg  
 41       35               40                   45  
 42 Cys Phe Gly Glu Ser Glu Val Ser Trp Gln Tyr Pro Met Ser Glu Glu  
 43       50               55                   60  
 44 Glu Ser Ser Asp Val Glu Ile Arg Asn Glu Glu Asn Asn Ser Gly Leu  
 45       65               70                   75                   80  
 46 Phe Val Thr Val Leu Glu Val Ser Ser Ala Ser Ala Ala His Thr Gly  
 47       85               90                   95  
 48 Leu Tyr Thr Cys Tyr Tyr Asn His Thr Gln Thr Glu Glu Asn Glu Leu  
 49       100              105                   110  
 50 Glu Gly Arg His Ile Tyr Ile Tyr Val Pro Asp Pro Asp Val Ala Phe  
 51       115              120                   125  
 52 Val Pro Leu Gly Met Thr Asp Tyr Leu Val Ile Val Glu Asp Asp Asp  
 53       130              135                   140  
 54 Ser Ala Ile Ile Pro Cys Arg Thr Thr Asp Pro Glu Thr Pro Val Thr  
 55       145              150                   155                   160  
 56 Leu His Asn Ser Glu Gly Val Val Pro Ala Ser Tyr Asp Ser Arg Gln

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59	180	185	190
60	Val Lys Gly Lys Lys Phe Gln Thr Ile Pro Phe Asn Val Tyr Ala Leu		
61	195	200	205
62	Lys Ala Thr Ser Glu Leu Asp Leu Glu Met Glu Ala Leu Lys Thr Val		
63	210	215	220
64	Tyr Lys Ser Gly Glu Thr Ile Val Val Thr Cys Ala Val Phe Asn Asn		
65	225	230	235
66	Glu Val Val Asp Leu Gln Trp Thr Tyr Pro Gly Glu Val Lys Gly Lys		
67	245	250	255
68	Gly Ile Thr Met Leu Glu Glu Ile Lys Val Pro Ser Ile Lys Leu Val		
69	260	265	270
70	Tyr Thr Leu Thr Val Pro Glu Ala Thr Val Lys Asp Ser Gly Asp Tyr		
71	275	280	285
72	Glu Cys Ala Ala Arg Gln Ala Thr Arg Glu Val Lys Glu Met Lys Lys		
73	290	295	300
74	Val Thr Ile Ser Val His Glu Lys Gly Phe Ile Glu Ile Lys Pro Thr		
75	305	310	315
76	Phe Ser Gin Leu Glu Ala Val Asn Leu His Glu Val Lys His Phe Val		
77	325	330	335
78	Val Glu Val Arg Ala Tyr Pro Pro Arg Ile Ser Trp Leu Lys Asn		
79	340	345	350
80	Asn Leu Thr Leu Ile Glu Asn Leu Thr Glu Ile Thr Thr Asp Val Glu		
81	355	360	365
82	Lys Ile Gln Glu Ile Arg Tyr Arg Ser Lys Leu Lys Leu Ile Arg Ala		
83	370	375	380
84	Lys Glu Glu Asp Ser Gly His Tyr Thr Ile Val Ala Gln Asn Glu Asp		
85	385	390	395
86	Ala Val Lys Ser Tyr Thr Phe Glu Leu Leu Thr Gln Val Pro Ser Ser		
87	405	410	415
88	Ile Leu Asp Leu Val Asp Asp His His Gly Ser Thr Gly Gly Gln Thr		
89	420	425	430
90	Val Arg Cys Thr Ala Glu Gly Thr Pro Leu Pro Asp Ile Glu Trp Met		
91	435	440	445
92	Ile Cys Lys Asp Ile Lys Lys Cys Asn Asn Glu Thr Ser Trp Thr Ile		
93	450	455	460
94	Leu Ala Asn Asn Val Ser Asn Ile Ile Thr Glu Ile His Ser Arg Asp		
95	465	470	475
96	Arg Ser Thr Val Glu Gly Arg Val Thr Phe Ala Lys Val Glu Glu Thr		
97	485	490	495
98	Ile Ala Val Arg Cys Leu Ala Lys Asn Leu Leu Gly Ala Glu Asn Arg		
99	500	505	510
100	Glu Leu Lys Leu Val Ala Pro Thr Leu Arg Ser Glu Leu Thr Val Ala		
101	515	520	525
102	Ala Ala Val Leu Val Leu Val Ile Val Ile Ile Ser Leu Ile Val		
103	530	535	540
104	Leu Val Val Ile Trp Lys Gln Lys Pro Arg Tyr Glu Ile Arg Trp Arg		
105	545	550	555
			560

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107 565 570 575  
108 Pro Met Gln Leu Pro Tyr Asp Ser Arg Trp Glu Phe Pro Arg Asp Gly  
109 580 585 590  
110 Leu Val Leu Gly Arg Val Leu Gly Ser Gly Ala Phe Gly Lys Val Val  
111 595 600 605  
112 Glu Gly Thr Ala Tyr Gly Leu Ser Arg Ser Gln Pro Val Met Lys Val  
113 610 615 620  
114 Ala Val Lys Met Leu Lys Pro Thr Ala Arg Ser Ser Glu Lys Gln Ala  
115 625 630 635 640  
116 Leu Met Ser Glu Leu Lys Ile Met Thr His Leu Gly Pro His Leu Asn  
117 645 650 655  
118 Ile Val Asn Leu Leu Gly Ala Cys Thr Lys Ser Gly Pro Ile Tyr Ile  
119 660 665 670  
120 Ile Thr Glu Tyr Cys Phe Tyr Gly Asp Leu Val Asn Tyr Leu His Lys  
121 675 680 685  
122 Asn Arg Asp Ser Phe Leu Ser His His Pro Glu Lys Pro Lys Lys Glu  
123 690 695 700  
124 Leu Asp Ile Phe Gly Leu Asn Pro Ala Asp Glu Ser Thr Arg Ser Tyr  
125 705 710 715 720  
126 Val Ile Leu Ser Phe Glu Asn Asn Gly Asp Tyr Met Asp Met Lys Gln  
127 725 730 735  
128 Ala Asp Thr Thr Gln Tyr Val Pro Met Leu Glu Arg Lys Glu Val Ser  
129 740 745 750  
130 Lys Tyr Ser Asp Ile Gln Arg Ser Leu Tyr Asp Arg Pro Ala Ser Tyr  
131 755 760 765  
132 Lys Lys Ser Met Leu Asp Ser Glu Val Lys Asn Leu Leu Ser Asp  
133 770 775 780  
134 Asp Asn Ser Glu Gly Leu Thr Leu Asp Leu Leu Ser Phe Thr Tyr  
135 785 790 795 800  
136 Gln Val Ala Arg Gly Met Glu Phe Leu Ala Ser Lys Asn Cys Val His  
137 805 810 815  
138 Arg Asp Leu Ala Ala Arg Asn Val Leu Leu Ala Gln Gly Lys Ile Val  
139 820 825 830  
140 Lys Ile Cys Asp Phe Gly Leu Ala Arg Asp Ile Met His Asp Ser Asn  
141 835 840 845  
142 Tyr Val Ser Lys Gly Ser Thr Phe Leu Pro Val Lys Trp Met Ala Pro  
143 850 855 860  
144 Glu Ser Ile Phe Asp Asn Leu Tyr Thr Leu Ser Asp Val Trp Ser  
145 865 870 875 880  
146 Tyr Gly Ile Leu Leu Trp Glu Ile Phe Ser Leu Gly Gly Thr Pro Tyr  
147 885 890 895  
148 Pro Gly Met Met Val Asp Ser Thr Phe Tyr Asn Lys Ile Lys Ser Gly  
149 900 905 910  
150 Tyr Arg Met Ala Lys Pro Asp His Ala Thr Ser Glu Val Tyr Glu Ile  
151 915 920 925  
152 Met Val Lys Cys Trp Asn Ser Glu Pro Glu Lys Arg Pro Ser Phe Tyr  
153 930 935 940  
154 His Leu Ser Glu Ile Val Glu Asn Leu Leu Pro Gly Gln Tyr Lys Lys

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155 945 950 955 960  
156 Ser Tyr Glu Lys Ile His Leu Asp Phe Leu Lys Ser Asp His Pro Ala  
157 965 970 975  
158 Val Ala Arg Met Arg Val Asp Ser Asp Asn Ala Tyr Ile Gly Val Thr  
159 980 985 990  
160 Tyr Lys Asn Glu Glu Asp Lys Leu Lys Asp Trp Glu Gly Gly Leu Asp  
161 995 1000 1005  
162 Glu Gln Arg Leu Ser Ala Asp Ser Gly Tyr Ile Ile Pro Leu Pro Asp  
163 1010 1015 1020  
164 Ile Asp Pro Val Pro Glu Glu Asp Leu Gly Lys Arg Asn Arg His  
165 1025 1030 1035 1040  
166 Ser Ser Gln Thr Ser Glu Glu Ser Ala Ile Glu Thr Gly Ser Ser Ser  
167 1045 1050 1055  
168 Ser Thr Phe Ile Lys Arg Glu Asp Glu Thr Ile Glu Asp Ile Asp Met  
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187 gagaagtttc ccagagctat ggggacttcc catccggcgt tcctggtctt aggctgtctt 180  
188 ctcacaggcc tgagcctaattt cctctgccag ctttcattac cctctatctt tccaaatgaa 240  
189 aatgaaaagg ttgtgcagct gaattcatcc ttttctctga gatgcttgg ggagagtgaa 300  
190 gtgagctggc agtaccccat gtctgaagaa gagagctccg atgtggaaat cagaaatgaa 360  
191 gaaaacaaca gcggcctttt tggacggtc ttggaaatgtga gcagtgcctc ggcggcccac 420  
192 acagggttgt acacttgcta ttacaaccac actcagacag aagagaatgaa gcttgaaggc 480  
193 aggacacatt acatctatgt gccagaccca gatgtgcctt ttgtacctctt aggaatgacg 540  
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202 gctaccaggagg aggtcaaaga aatgaagaaa gtcactattt ctgtccatgtt gaaaggtttc 1080  
203 attgaaaatca aacccacattt cagccagttt gaaatgttca acctgcattt gtttgcattt 1140  
204 tttgtttagt aggtgcgggc ctaccacccat cccaggatattt cctggctgaa aaacaatctg 1200  
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206 tatcgttcaaaa aattaaagct gatccgttca aaggttcaag acaatgttca ttataactattt 1320  
207 gtagctcaaaa atgttcaaaa aactgttcaac tcaagtttcc 1380

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211	gagatccact	cccgagacag	gagtaccgtg	gagggccgtg	tgactttcgc	caaagtggag	1620
212	gagaccatcg	ccgtgcgtg	cctggctaag	aatctcctt	gagctgagaa	ccgagagctg	1680
213	aagctgggg	ctcccaccct	gcgttctgaa	ctcacggtg	ctgctgcagt	cctggtgctg	1740
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215	tatgaaattc	gctggagggt	cattgaatca	atcagcccg	atggacatga	atatatttat	1860
216	gtggacccga	tgcagctgcc	ttatgactca	agatgggagt	ttccaagaga	tggacttagt	1920
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